M E

#2

```
            RAW SEQUENCE LISTING              DATE: 04/26/2001
            PATENT APPLICATION:  US/09/769,970   TIME: 17:20:02

            Input Set : N:\Crf3\RULE60\09769970.txt
            Output Set: N:\CRF3\04262001\I769970.raw

            SEQUENCE LISTING
C-->  3 (1) GENERAL INFORMATION:
      5       (i) APPLICANT: Bandman, Olga
      6                      Hillman, Jennifer L.
      7                      Corley, Neil C.
      8                      Guegler, Karl G.
      9                      Lal, Preeti
     10                      Goli, Surya K.
     11                      Shah, Purvi
C--> 13      (ii) TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
     14                               KINASES
     16     (iii) NUMBER OF SEQUENCES: 21
     18      (iv) CORRESPONDENCE ADDRESS:
     19           (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
     20           (B) STREET: 3174 Porter Drive
     21           (C) CITY: Palo Alto
     22           (D) STATE: CA
     23           (E) COUNTRY: USA
     24           (F) ZIP: 94304
     26       (v) COMPUTER READABLE FORM:
     27           (A) MEDIUM TYPE: Diskette
     28           (B) COMPUTER: IBM Compatible
     29           (C) OPERATING SYSTEM: DOS
     30           (D) SOFTWARE: FastSEQ for Windows Version 2.0
     32      (vi) CURRENT APPLICATION DATA:
C--> 33           (A) APPLICATION NUMBER: US/09/769,970
C--> 34           (B) FILING DATE: 24-Jan-2001
     35           (C) CLASSIFICATION:
     37     (vii) PRIOR APPLICATION DATA:
     38           (A) APPLICATION NUMBER: 09/272,796
     39           (B) FILING DATE:
     43    (viii) ATTORNEY/AGENT INFORMATION:
     44           (A) NAME: Billings, Lucy J J
     45           (B) REGISTRATION NUMBER: 36,749
     46           (C) REFERENCE/DOCKET NUMBER: PF-0321 US
     48      (ix) TELECOMMUNICATION INFORMATION:
     49           (A) TELEPHONE: 415-855-0555
     50           (B) TELEFAX: 415-845-4166
     51           (C) TELEX:
     54 (2) INFORMATION FOR SEQ ID NO: 1:
     56       (i) SEQUENCE CHARACTERISTICS:
     57           (A) LENGTH: 685 amino acids
     58           (B) TYPE: amino acid
     59           (C) STRANDEDNESS: single
     60           (D) TOPOLOGY: linear
     62     (vii) IMMEDIATE SOURCE:
     63           (A) LIBRARY: HUVENOB01
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ENTERED

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                  RAW SEQUENCE LISTING              DATE: 04/26/2001
                  PATENT APPLICATION:  US/09/769,970  TIME: 17:20:02

                  Input Set : N:\Crf3\RULE60\09769970.txt
                  Output Set: N:\CRF3\04262001\I769970.raw
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 64            (B) CLONE: 39043
 66     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 68    Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys
 69    1               5               10              15
 70    Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys
 71            20              25              30
 72    Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
 73            35              40              45
 74    Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His
 75        50              55              60
 76    Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
 77    65              70              75              80
 78    Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
 79                85              90              95
 80    Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
 81            100             105             110
 82    Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp
 83            115             120             125
 84    Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
 85        130             135             140
 86    Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
 87    145             150             155             160
 88    Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
 89                165             170             175
 90    Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
 91            180             185             190
 92    Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu
 93            195             200             205
 94    Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe
 95.       210             215             220
 96    Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile
 97    225             230             235             240
 98    Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly
 99                245             250             255
100    His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr
101                260             265             270
102    Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr
103            275             280             285
104    Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu
105        290             295             300
106    Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu
107    305             310             315             320
108    Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln
109                325             330             335
110    Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro
111            340             345             350
112    Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala
113            355             360             365
114    Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr
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RAW SEQUENCE LISTING   DATE: 04/26/2001
PATENT APPLICATION: US/09/769,970   TIME: 17:20:02
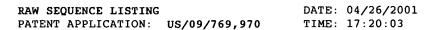
Input Set : N:\Crf3\RULE60\09769970.txt
Output Set: N:\CRF3\04262001\I769970.raw

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115     370                     375                 380
116     His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His
117     385                     390                 395                 400
118     Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr
119                     405                 410                 415
120     Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr
121                 420                 425                 430
123     Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
124             435                 440                 445
125     Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
126         450                 455                 460
127     Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
128     465                 470                 475                 480
129     Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
130                 485                 490                 495
131     Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
132                 500                 505                 510
133     Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
134             515                 520                 525
135     Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Ala
136         530                 535                 540
137     His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
138     545                 550                 555                 560
139     Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
140                 565                 570                 575
141     His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
142             580                 585                 590
143     Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
144             595                 600                 605
145     Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
146         610                 615                 620
147     Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
148     625                 630                 635                 640
149     Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
150             645                 650                 655
151     Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
152             660                 665                 670
153     Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
154         675                 680                 685
156  (2) INFORMATION FOR SEQ ID NO: 2:
158      (i) SEQUENCE CHARACTERISTICS:
159          (A) LENGTH: 448 amino acids
160          (B) TYPE: amino acid
161          (C) STRANDEDNESS: single
162          (D) TOPOLOGY: linear
164    (vii) IMMEDIATE SOURCE:
165          (A) LIBRARY: TBLYNOT01
166          (B) CLONE: 40194
168     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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170   Met Pro Pro Lys Arg Asn Glu Lys Tyr Lys Leu Pro Ile Pro Phe Pro
171   1                   5                  10                  15
172   Glu Gly Lys Val Leu Asp Asp Met Glu Gly Asn Gln Trp Val Leu Gly
173               20                  25                  30
174   Lys Lys Ile Gly Ser Gly Gly Phe Gly Leu Ile Tyr Leu Ala Phe Pro
175           35                  40                  45
176   Thr Asn Lys Pro Glu Lys Asp Ala Arg His Val Val Lys Val Glu Tyr
177       50                  55                  60
178   Gln Glu Asn Gly Pro Leu Phe Ser Glu Leu Lys Phe Tyr Gln Arg Val
179   65                  70                  75                  80
180   Ala Lys Lys Asp Cys Ile Lys Lys Trp Ile Glu Arg Lys Gln Leu Asp
181               85                  90                  95
183   Tyr Leu Gly Ile Pro Leu Phe Tyr Gly Ser Gly Leu Thr Glu Phe Lys
184               100                 105                 110
185   Gly Arg Ser Tyr Arg Phe Met Val Met Glu Arg Leu Gly Ile Asp Leu
186           115                 120                 125
187   Gln Lys Ile Ser Gly Gln Asn Gly Thr Phe Lys Lys Ser Thr Val Leu
188           130                 135                 140
189   Gln Leu Gly Ile Arg Met Leu Asp Val Leu Glu Tyr Ile His Glu Asn
190   145                 150                 155                 160
191   Glu Tyr Val His Gly Asp Val Lys Ala Ala Asn Leu Leu Leu Gly Tyr
192               165                 170                 175
193   Lys Asn Pro Asp Gln Val Tyr Leu Ala Asp Tyr Gly Leu Ser Tyr Arg
194               180                 185                 190
195   Tyr Cys Pro Asn Gly Asn His Lys Gln Tyr Gln Glu Asn Pro Arg Lys
196           195                 200                 205
197   Gly His Asn Gly Thr Ile Glu Phe Thr Ser Leu Asp Ala His Lys Gly
198       210                 215                 220
199   Val Gly Glu Ile Ala Gln Phe Leu Val Cys Ala His Ser Leu Ala Tyr
200   225                 230                 235                 240
201   Asp Glu Lys Pro Asn Tyr Gln Ala Leu Lys Lys Ile Leu Asn Pro His
202               245                 250                 255
203   Gly Ile Pro Leu Gly Pro Leu Asp Phe Ser Thr Lys Gly Gln Ser Ile
204               260                 265                 270
205   Asn Val His Thr Pro Asn Ser Gln Lys Val Asp Ser Gln Lys Ala Ala
206        275                 280                 285
207   Thr Lys Gln Val Asn Lys Ala His Asn Arg Leu Ile Glu Lys Lys Val
208       290                 295                 300
209   His Ser Glu Arg Ser Ala Glu Ser Cys Ala Thr Trp Lys Val Gln Lys
210   305                 310                 315                 320
211   Glu Glu Lys Leu Ile Gly Leu Met Asn Asn Glu Ala Ala Gln Glu Ser
212               325                 330                 335
213   Thr Arg Arg Arg Gln Lys Tyr Gln Glu Ser Gln Glu Pro Leu Asn Glu
214               340                 345                 350
215   Val Asn Ser Phe Pro Gln Lys Ile Ser Tyr Thr Gln Phe Pro Asn Ser
216           355                 360                 365
217   Phe Tyr Glu Pro His Gln Asp Phe Thr Ser Pro Asp Ile Phe Lys Lys
218       370                 375                 380
219   Ser Arg Ser Pro Ser Trp Tyr Lys Tyr Thr Ser Thr Val Ser Thr Gly
```

```
220  385                    390                    395                    400
221  Ile Thr Asp Leu Glu Ser Ser Thr Gly Leu Trp Pro Thr Ile Ser Gln
222                  405                    410                    415
223  Phe Thr Leu Ser Glu Glu Thr Asn Ala Asp Val Tyr Tyr Tyr Arg Ile
224                  420                    425                    430
225  Ile Ile Pro Val Leu Leu Met Leu Val Phe Leu Ala Leu Phe Phe Leu
226                  435                    440                    445
228  (2) INFORMATION FOR SEQ ID NO: 3:
230       (i) SEQUENCE CHARACTERISTICS:
231           (A) LENGTH: 400 amino acids
232           (B) TYPE: amino acid
233           (C) STRANDEDNESS: single
234           (D) TOPOLOGY: linear
236      (vii) IMMEDIATE SOURCE:
237           (A) LIBRARY: TMLR3DT01
238           (B) CLONE: 402339
240      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
242  Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro
243  1               5                   10                  15
244  Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala
245                  20                  25                  30
246  Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
247                  35                  40                  45
248  Gln Gln Lys Lys Arg Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val
249       50                  55                  60
250  Gly Glu Leu Lys Asp Asp Asp Phe Glu Arg Ile Ser Glu Leu Gly Ala
251  65                  70                  75                  80
252  Gly Asn Gly Gly Val Val Thr Lys Val Gln His Arg Pro Ser Gly Leu
253                  85                  90                  95
254  Ile Met Ala Arg Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg
255                  100                 105                 110
256  Asn Gln Ile Ile Arg Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro
257       115                 120                 125
258  Tyr Ile Val Gly Phe Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser
259       130                 135                 140
260  Ile Cys Met Glu His Met Asp Gly Gly Ser Leu Asp His Leu Leu Lys
261  145                 150                 155                 160
262  Glu Ala Lys Arg Ile Pro Glu Glu Ile Leu Gly Lys Val Ser Ile Ala
263                  165                 170                 175
264  Val Leu Arg Gly Leu Ala Tyr Leu Arg Glu Lys His Gln Ile Met His
265                  180                 185                 190
266  Arg Asp Val Lys Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile
267       195                 200                 205
268  Lys Leu Cys Asp Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala
269       210                 215                 220
270  Asn Ser Phe Val Gly Thr Arg Ser Tyr Met Ala Pro Glu Arg Leu Gln
271  225                 230                 235                 240
272  Gly Thr His Tyr Ser Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser
273                  245                 250                 255
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/769,970

DATE: 04/26/2001
TIME: 17:20:04

Input Set : N:\Crf3\RULE60\09769970.txt
Output Set: N:\CRF3\04262001\I769970.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:13 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5